

Figure 1A

1 CAAGGTTCTGAAGGAAACAAGGTCAAGAGGACATCCTGCATGTATGGGGCAAACCTGCTAT 60

61 AGGAAGAATCCTGTTTCATTTTCAACATTTTAGCCATCCTGGTGATAGTGATTATGGAGGT 120

121 GTACAAATCGTGGGCCAAGATGAGACTGATGACCGGCCTGAATGTCCCTATGGACCATCC 180

181 TGTTATAGGAAGAATCCCCAGCACAAAGATAGAATATAGACATAATACGCTTCCAGTGAGA 240

241 AATGTTTTAGATGAAGATAATGATAATGTTGGGCAACCCAATGAGTATGACCTGAACGAC 300

301 AGCTTTCTAGATGATGAGGAAGAAGACTATGAGCCAACAGATGAAGATTCTGACTGGGAA 360

361 CCAGGAAAGGAAGATGAAGAGAAGGAAGATGTGGAAGAGCTTTTGAAAGAAGCAAAAAGC 420

421 AAATAATTTCCCGCATCTTCACTCTTCATCTTCCACCCTCTTCTGGACAACCTCCTGACA 480

481 TTCTGTGATATTCAGCATTACCCATAAACATTGCATGATTCAGTTCTCCTTGATATCTTG 540

541 GTGCTTGGACTCTTCACTGTTGGCATCATTAGGTCAGCAGGTGAACACTCAGGATTGTTT 600

601 CTCTTCTGTTAGTAGAGCACAAAAGACAGGGTCTGGCTCTGTACCTAAGCCAGAGGGC 660

661 AATGGTACAATCACCATTGACTGCAGTCTCAAATTCCTGGGCTCAAGCAATCCTCCCGCC 720

721 TCAGCTTCCCAAGCAGCTGGGACTACAGGCATGCCCCACCATGTCCAGGGAATGGTGTCT 780

781 GGACCCAGAGAATAACTGGATCTTCAAGGAAGGAAGAGAAATCTTCAGAAGAACATGGAT 840

841 TTTCCCCACTGGTAGTTAGTTGTCTCTTCCATATCCAGAAATAACTTGAACACGTTAGAC 900

901 GGGGCCACTGTGCATAGTGTCTCCAGGAAAACGCCAAGATTCTCCAAGACACTTTCAT 960

961 ATCCTAAGCCCTGTTCTGTTTGTCTTGTGTAGTAAATTGGCAAATTTGGCAGTACAGAA 1020

1021 GACATCTCTAACCTGATGTACAAAGAATCATGTCTGGCCCATACAAAGTATTCTAACTA 1080

1081 ACCATGTAAGCCACTAGAAATGTTAACTAATGCTCTGGCACTGAGGTTTAGAATGGAGCT 1140

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Figure 1B

1141 CAGATACCATAACCCCAAAGATGCTGGCAGAGACATTCTGACTCATTAAAGGGAGAGCTGGC 1200

1201 TGATAGCAGAGAGGGGTGACATCAGCCTTGACAGACATTGCCCTGGGGAATTCTGAGCAGT 1260

1261 GTTGCTCACAGCACCACTGGCCAGATGGAGACCACCATGGGGTTCATGGATGACAATGC 1320  
 1 M E T T M G F M D D N A 12

1321 CACCAACACTTCCACCAGCTTCCTTTCTGTGCTCAACCCTCATGGAGCCCATGCCACTTC 1380  
 13 T N T S T S F L S V L N P H G A H A T S 32

1381 CTTCCCATTCAACTTCAGCTACAGCGACTATGATATGCCTTTGGATGAAGATGAGGATGT 1440  
 33 F P F N F S Y S D Y D M P L D E D E D V 52

1441 GACCAATTCCAGGACGTTCTTTGCTGCCAAGATTGTCATTGGGATGGCCCTGGTGGGCAT 1500  
 53 T N S R T F F A A K I V I G M A L V G I 72

1501 CATGCTGGTCTGCGGCATTGGAACTTCATCTTTATCGCTGCCCTGGTCCGCTACAAGAA 1560  
 73 M L V C G I G N F I F I A A L V R Y K K 92

1561 ACTGCGCAACCTCACCAACCTGCTCATCGCCAACCTGGCCATCTCTGACTTCCTGGTGGC 1620  
 93 L R N L T N L L I A N L A I S D F L V A 112

1621 CATTGTCTGCTGCCCCCTTTGAGATGGACTACTATGTGGTGCGCCAGCTCTCCTGGGAGCA 1680  
 113 I V C P F E M D Y Y V V R Q L S W E H 132

1681 CGGCCACGTCCTGTGCACCTCTGTCAACTACCTGCGCACTGTCTCTCTCTATGTCTCCAC 1740  
 133 G H V L T S V N Y L R T V S L Y V S T 152

1741 CAATGCCCTGCTGGCCATCGCCATTGACAGGTATCTGGCTATTGTCCATCCGCTGAGACC 1800  
 153 N A L L A I A I D R Y L A I V H P L R P 172

1801 ACGGATGAAGTGCCAAACAGCCACTGGCCTGATTGCCTTGGTGTGGACGGTGTCCATCCT 1860  
 173 R M K C Q T A T G L I A L V W T V S I L 192


1861 GATCGCCATCCCTTCCGCCTACTTCACCACCGAGACGGTCCTCGTCATTGTCAAGAGCCA 1920  
 193 I A I P S A Y F T T E T V L V I V K S Q 212

1921 GGAAAAGATCTTCTGCGGCAGATCTGGCCTGTGGACCAGCTCTACTACAAGTCCTA 1980  
 213 E K I F G Q I W P V D Q Q L Y Y K S Y 232

1981 CTTCTCTTTATCTTTGGCATAGAATTCGTGGGCCCCGTGGTCACCATGACCCTGTGCTA 2040  
 233 F L F I F G I E F V G P V V T M T L C Y 252

10067649.02004

Figure 1C

2041	TGCCAGGATCTCCCGGGAGCTCTGGTTCAAGGCGGTCCCTGGATTCCAGACAGAGCAGAT	2100
253	<u>A</u> R I S R E L W F K A V P G F Q T E Q I	272
2101	CCGCAAGAGGCTGCGCTGCCGCAGGAAGACGGTCCTGGTGCTCATGTGCATCCTCACC GC	2160
273	R K R L R <b>C</b> R R K <u>T V L V L M</u>  I L T A	292
2161	CTACGTGCTATGCTGGGCGCCCTTCTACGGCTTCACCATCGTCGCGACTTCTTCCCCAC	2220
293	<u>Y V L C W A P F Y</u> G F T I V R D F F P T	312
2221	CGTGTTTGTAAAGGAGAAGCACTACCTCACTGCCTTCTACATCGTCGAGTGCATCGCCAT	2280
313	V F V K E K H Y L <u>T A F Y I V E C I A M</u>	332
2281	GAGCAACAGCATGATCAACACTCTGTGCTTCGTGACCGTCAAGAACGACACCGTCAAGTA	2340
333	<u>S N S M I N T L C F V T V</u> K N D T V K Y	352
2341	CTTCAAAAAGATCATGTTGCTCCACTGGAAGGCTTCTTACAATGGCGGTAAGTCCAGTGC	2400
353	F K K I M L L H W K A S Y N G G K S S A	372
2401	AGACCTGGACCTCAAGACAATTGGGATGCCTGCCACCGAAGAGGTGGACTGCATCAGACT	2460
373	D L D L K T I G M P A T E E V D C I R L	392
2461	AAAATAACCCCTGGACTTTGCAAAGTTTAAACACAAAGCAGGGTCCTGTGGACACTGAC	2520
393	K *	394
2521	TAGTGTGCTTGGATGCACATCAACCTGGAACCTTTTTGTTTGTCTGCAGAGGGTAAAGTAAA	2580
2581	TGGACCACTCTGTGAAA	2640
2641	AAAAAAAAAAAAAA	2654

20520" 6492900T

Figure 2

HGPRBMY14 METTMC~~GFMD~~DDN~~ATNT~~ST~~ST~~SV~~LN~~PHGAHATSFPFN~~SYSDYD~~MP~~LDE~~ED~~VT~~NSRTFFA  
 human\_gpcr\_dJ680N4\_3 ~~~~~~~~YCDYD~~LP~~DE~~ED~~VT~~TK~~RT~~FFA  
 gpr73\_mouse METTMCALGENTTT~~FT~~DDFSALDGH~~EAQ~~TGSLPFT~~SYCDYD~~MP~~LDE~~ED~~VT~~NSRTFFA  
 NPY2R\_chicken ~~~~MCPL~~EAL~~CE~~NC~~IDE~~MM~~....ELFTKLYLPRAT~~TPVSE~~LALDPKPELKDSTLVE  
 NPY2R\_rat ~~~~MCPLGA~~AD~~EN~~CT~~VE~~NKV~~....ELYGS..GP..TPRGE~~LPPD~~PE~~LID~~STKLVE

HGPRBMY14 AKIVIGMALVGIMLVCGIGNE~~FFIAAL~~RYKKLRNLTNLLIANLAISDFLVA~~ICCCPFEM~~  
 human\_gpcr\_dJ680N4\_3 AKIVIGMALAGIMLVCGIGNE~~FFIAAL~~TRYKKLRNLTNLLIANLAISDFLVA~~ICCCPFEM~~  
 gpr73\_mouse AKIVIGMALVGIMLVCGIGNE~~FFIT~~ALARYKKLRNLTNLLIANLAISDFLVA~~ICCCPFEM~~  
 NPY2R\_chicken VCH~~IL~~IFAYCS~~IL~~LGVI~~GN~~SLVIHVL~~IK~~SMRT~~VT~~NFFIANLAVADLLVNT~~ICLP~~ETI  
 NPY2R\_rat VQV~~VL~~ILIFAYCS~~IL~~LGVI~~GN~~SLVIHVL~~IK~~SMRT~~VT~~NFFIANLAVADLLVNT~~ICLP~~ETI

HGPRBMY14 DYYVVVRLSWEHGHVLC~~TSVNYL~~RTVSLYVSTNALLAIAIDRYLAIVHPL~~PRMKCOT~~AT  
 human\_gpcr\_dJ680N4\_3 DYYVVVRLSWEHGHVLCASVNYLRTVSLYVSTNALLAIAIDRYLAIVHPL~~PRMKCOT~~AS  
 gpr73\_mouse DYYVVVRLSWEHGHVLCASVNYLRTVSLYVSTNALLAIAIDRYLAIVHPL~~PRMKCOT~~AA  
 NPY2R\_chicken VY~~TL~~LGGE..WKLGPVLC~~HL~~VPYAQA~~LAVH~~VSTVT~~TVIA~~DRHRCIVYHLES~~ISK~~RSKISF  
 NPY2R\_rat TY~~TL~~LGGE..WKMGPVLC~~HL~~VPYAQA~~LAVH~~VSTVT~~TVIA~~DRHRCIVYHLES~~ISK~~RSKISF

HGPRBMY14 GLIALVMTVSILIAIP~~SAYF~~TTETVLMIVKS~~OEKIF~~CGQIWPVDQQLYY~~YS~~.YFL~~FI~~FCI  
 human\_gpcr\_dJ680N4\_3 GLIALVMMVSILIAIP~~SAYF~~TTETVLMIVKS~~OEKIF~~CGQIWPVDQQLYY~~YS~~.YFL~~FI~~FCI  
 gpr73\_mouse GLIFLVMSVSILIAIP~~AA~~YF~~TT~~ETVLMIV~~ER~~OEKIFCGQIWPVDQQLYY~~YS~~.YFL~~LV~~FCI  
 NPY2R\_chicken LIL~~AV~~AVASALIAS~~PLA~~IREYSL~~TEI~~PDFKI~~VC~~SEK~~WPG~~CGQIN~~YCT~~IYVS~~SM~~LLI  
 NPY2R\_rat LIL~~AV~~AVASALIAS~~PLA~~IREYSL~~TEI~~PDF~~FEI~~MACTEK~~WPG~~SEKSV~~CT~~IYVS~~ST~~LLI

HGPRBMY14 EFVGPVVMTILCYARISRELWFKAVPGFQTEQIR~~RTR~~RCRRKT~~VLM~~MLC~~IL~~TAYVLCWAP  
 human\_gpcr\_dJ680N4\_3 EFVGPVVMTILCYARISRELWFKAVPGFQTEQIR~~RTR~~RCRRKT~~VLM~~MLC~~IL~~TAYVLCWAP  
 gpr73\_mouse EFVGPVVAMTILCYARISRELWFKAVPGFQTEQIR~~RTV~~RCRRKT~~VLM~~GLVCVLSAYVLCWAP  
 NPY2R\_chicken QYVLP~~LA~~ITSYATRI~~WT~~KLKNHVS~~PGAGN~~DHYHHR...R~~OK~~TKMLVCV~~VV~~EA~~VS~~WLP  
 NPY2R\_rat L~~AV~~LP~~GI~~TSFSYTRI~~WS~~KLKNHVS~~PGAAS~~DHYHOR...R~~HK~~TKMLVCV~~VV~~EA~~VS~~WLP

HGPRBMY14 FYGFTIVRDFFP~~SVFV~~KEKHYLTAFY~~VECI~~AMSNSMINTLCFVT~~VKN~~DMKYF.....  
 human\_gpcr\_dJ680N4\_3 FYGFTIVRDFFP~~SVFV~~KEKHYLTAFY~~VECI~~AMSNSMINTLCFVT~~VKN~~DMKYF.....  
 gpr73\_mouse FYGFTIVRDFFP~~SVFV~~KEKHYLTAFY~~VECI~~AMSNSMINTLCFVT~~VKN~~DMKYF.....  
 NPY2R\_chicken F~~HF~~Q~~V~~SDIDSQV.LDLKE~~Y~~KLI~~TV~~FHV~~IA~~MCST~~FAN~~PILY~~GW~~MNN~~NY~~RTA~~LTA~~FQC  
 NPY2R\_rat L~~HA~~FQ~~AV~~DIDSHV.LDLKE~~Y~~KLI~~TV~~FHV~~IA~~MCST~~FAN~~PILY~~GW~~MNS~~NY~~RTA~~LTA~~SAFRC

HGPRBMY14 .K~~SM~~LLH~~WK~~AS~~YNG~~GRSSADLDLKTIG~~PA~~TEEVDCIRLK  
 human\_gpcr\_dJ680N4\_3 .K~~SM~~LLH~~WR~~PS~~ORG~~SRSSADLDL~~ENG~~PTTEEVDCIRLK  
 gpr73\_mouse .K~~RI~~LR~~QWR~~AS~~PSG~~SKASADLDL~~RTG~~PA~~TE~~EVDCIRLK  
 NPY2R\_chicken EQR~~DS~~TH~~PE~~VSAA.FKARK~~KL~~EAKKSQ~~FP~~QDSFTQPTNV~  
 NPY2R\_rat EQR~~DA~~TH~~SE~~VSM~~T~~.FKAK~~KN~~LE~~VK~~KNGLTDSFS~~EAT~~NV~

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Figure 3

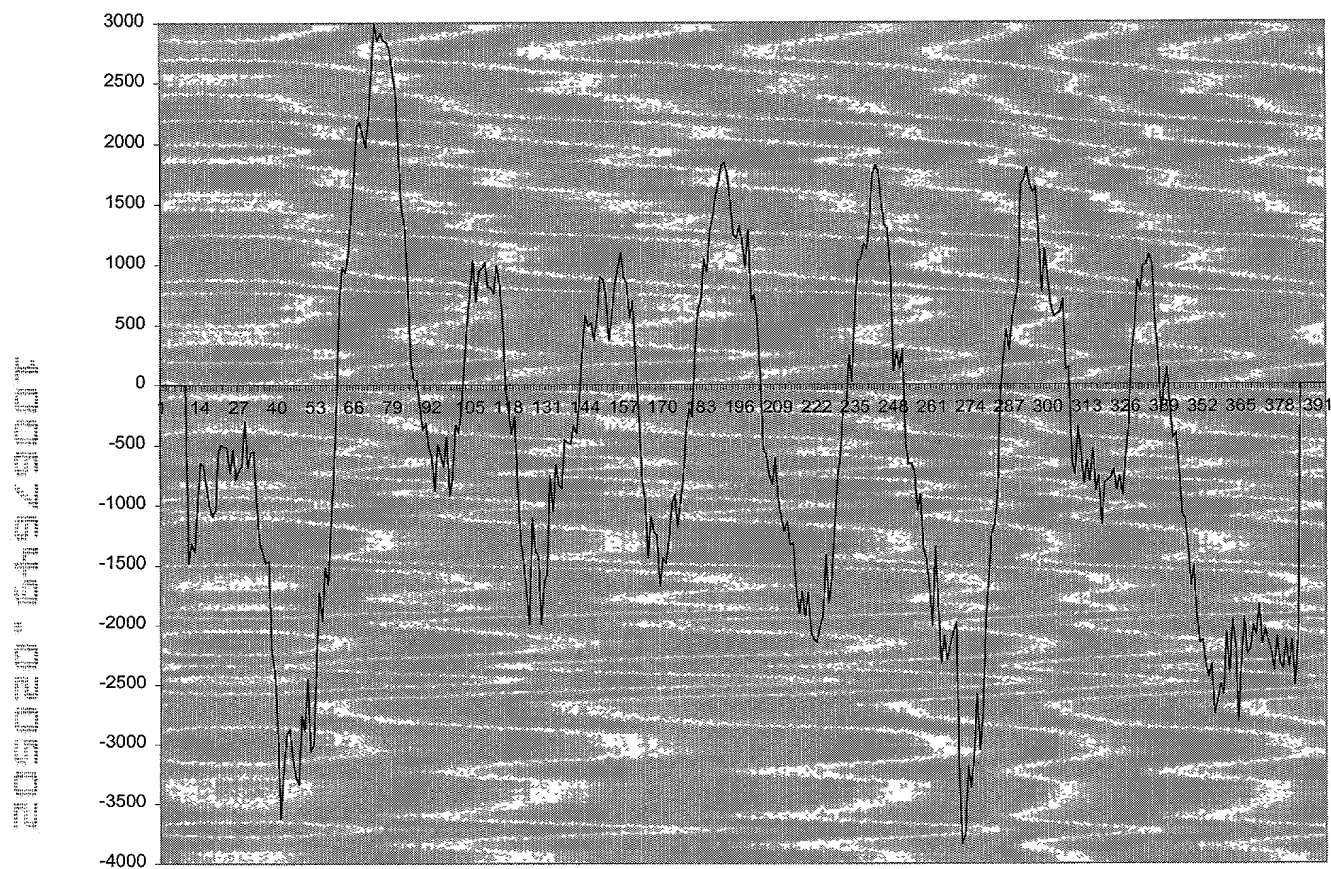


Figure 4

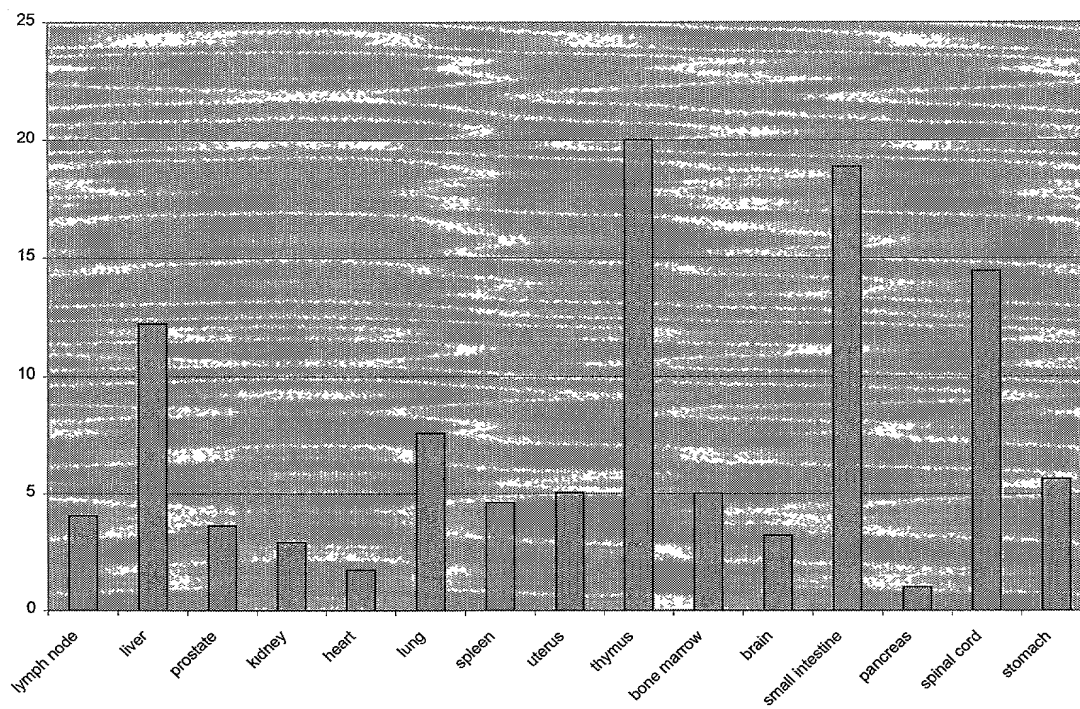
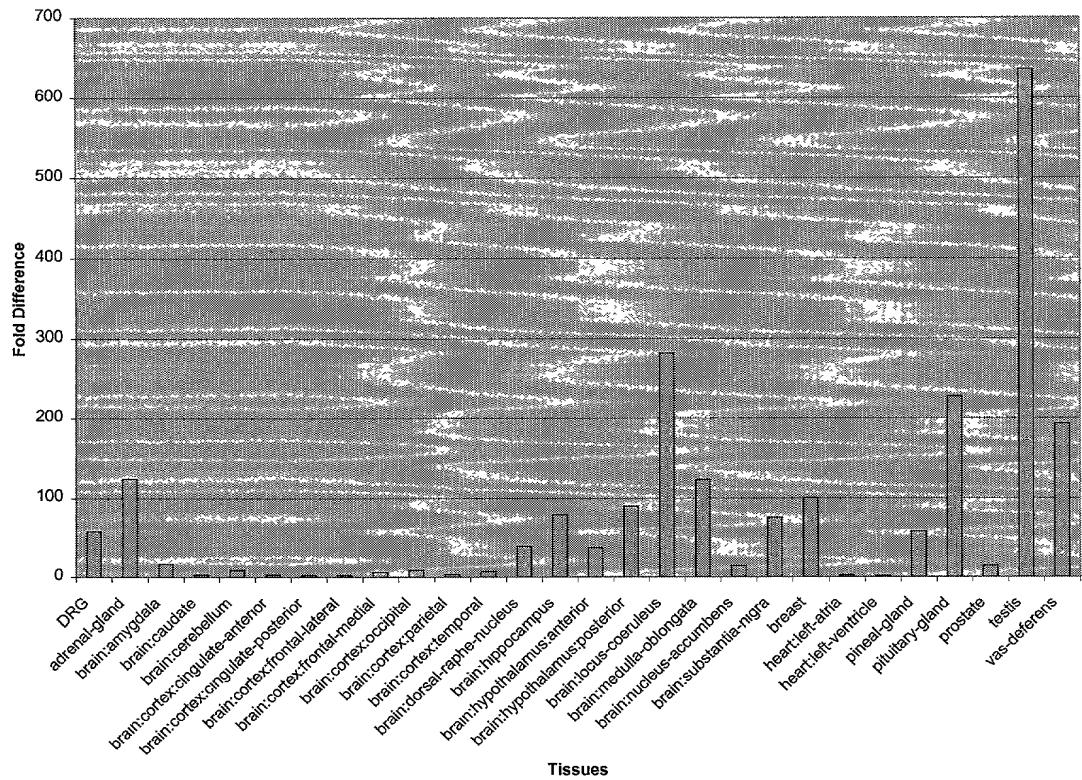


Figure 5.

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human dJ680N4.3 G-protein coupled receptor	gi 7688218	90%	93%
mouse G-protein coupled receptor GPR73 protein	gi 7248884	84%	88%
chicken neuropeptide Y receptor Y2 protein	gi 11545537	27%	39%
rat neuropeptide Y/peptide YY-Y2 receptor protein	gi 10281748	29%	41%

"05020" 6492900F

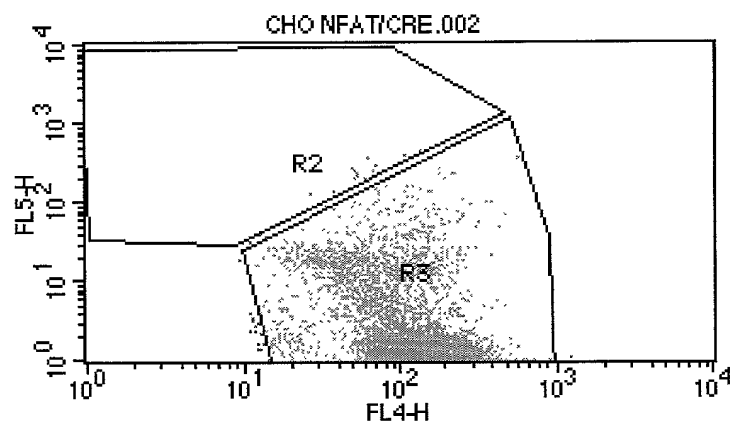
Figure 6



205020 6492900

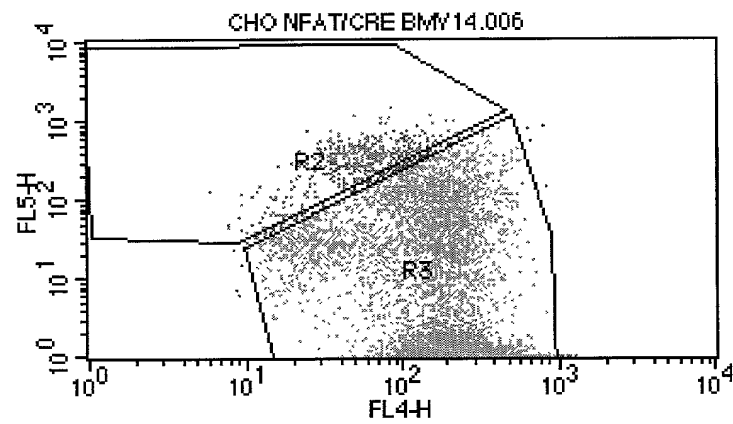


Figure 7



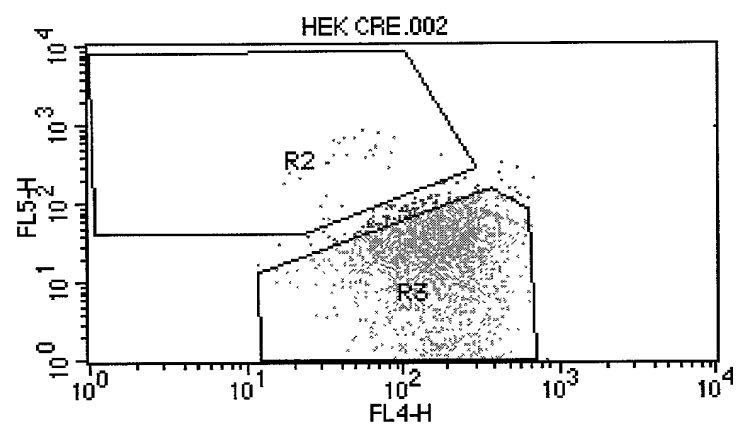
205020 649/5001

Figure 8



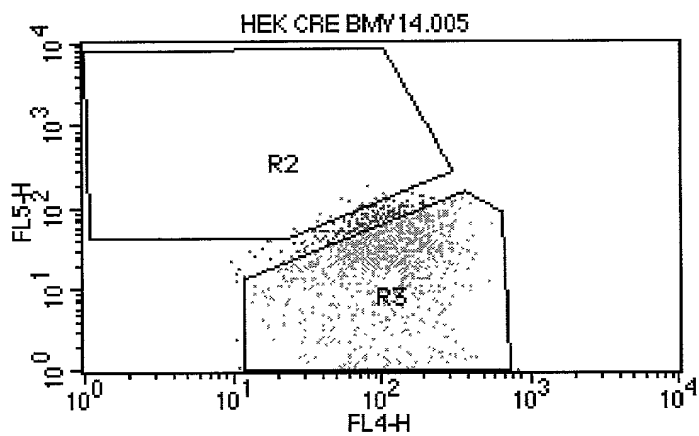
205020" 6494900F

Figure 9



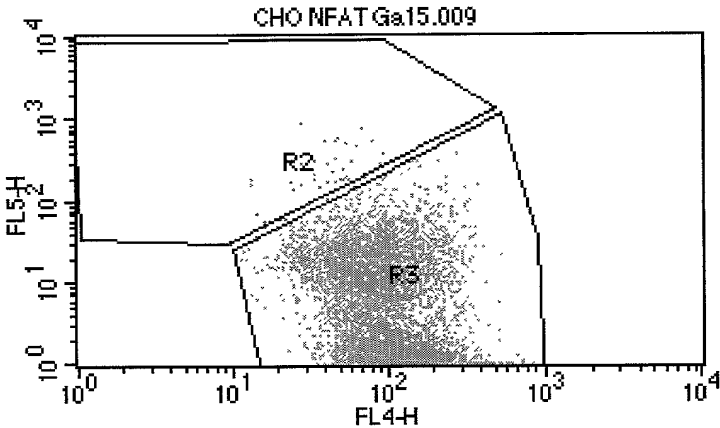
205020 64925001

Figure 10



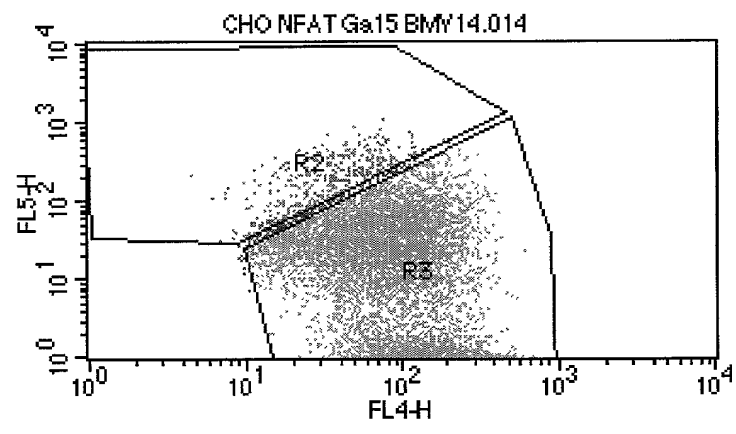
205020" 64925001

Figure 11



205020 6494900T

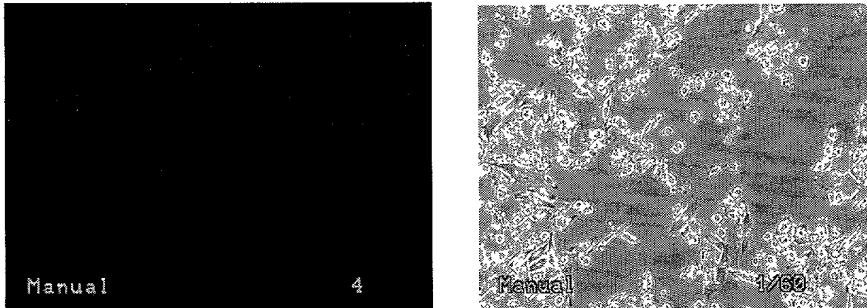
Figure 12



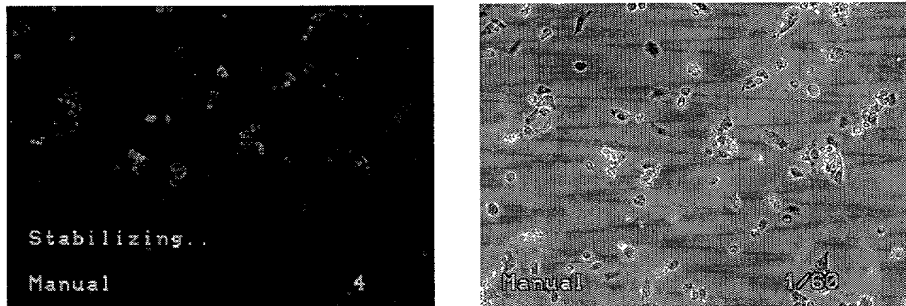
205020 6492900

Figure 13

Cho NFAT Ga15 Control (Fluorescent vs. Bright Field)



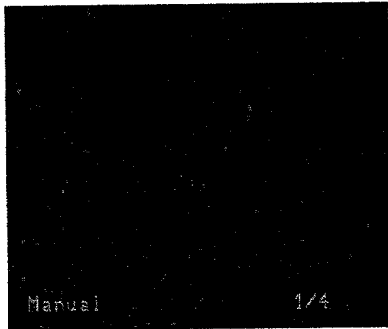
Cho NFAT Ga15 BMY14 (Fluorescent vs. Bright Field)



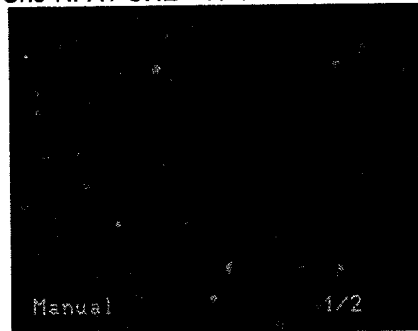
205020" 64979001

**Figure 14**

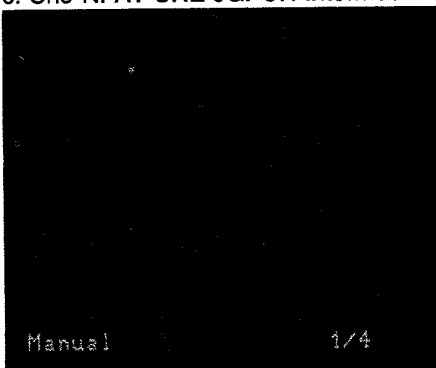
a. Cho-NFAT CRE



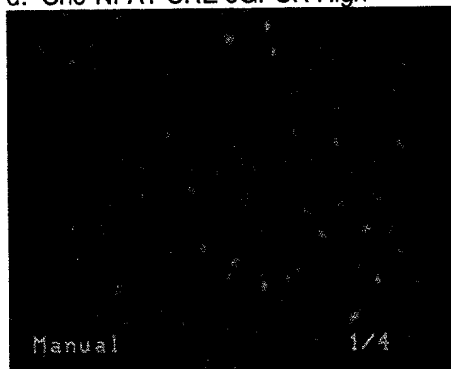
b. Cho-NFAT CRE + F/T/P



c. Cho-NFAT CRE oGPCR-Intermediate



d. Cho-NFAT CRE oGPCR High





**Figure 15**

VDT**F**EDIPWGFVLF (SEQ ID NO:87)  
**L**FVDK**W**DL**S**NFWGGG (SEQ ID NO:88)  
**L**F**L**E**A**WDLSDTPHLY (SEQ ID NO:89)  
VWGN**S**L**I**VGR**W**D**V**VG (SEQ ID NO:90)  
IGGV**G**D**G**LY**V**V**S**WDL (SEQ ID NO:91)